

¹
 IAP5 Rec'd PCT/PTO 10 FEB 2006
 SEQUENCE LISTING

<110> Wyeth
 Flannery, Carl R
 Corcoran, Christopher J
 Freeman, Bethany A
 Racie, Lisa A

<120> RECOMBINANT LUBRICIN MOLECULES AND USES THEREOF

<130> 50657-01404WOPT

<160> 29

<170> PatentIn version 3.3

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Thr Thr Pro
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<223> Nucleotide sequence of synthetic cDNA cassette-2.

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<223> Translation of SEQ ID NO: 3.

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<223> pTmed2 vector containing recombinant PRG4-Lub:1 cDNA construct.

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Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
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Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
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Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
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Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
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Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
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Ser Glu Asn Gln Glu Ser
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435	440	445	
Ser Pro Asp Glu Ser Thr Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys			
450	455	460	
Ala Leu Glu Asn Ser Pro Lys Glu Pro Gly Val Pro Thr Thr Lys Thr			
465	470	475	480
Pro Ala Ala Thr Lys Pro Glu Met Thr Thr Ala Lys Asp Lys Thr			
485	490	495	
Thr Glu Arg Asp Leu Arg Thr Thr Pro Glu Thr Thr Ala Ala Pro			
500	505	510	
Lys Met Thr Lys Glu Thr Ala Thr Thr Glu Lys Thr Thr Glu Ser			
515	520	525	

Lys Ile Thr Ala Thr Thr Gln Val Thr Ser Thr Thr Gln Asp
530 535 540

Thr Thr Pro Phe Lys Ile Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro
545 550 555 560

Lys Val Thr Thr Lys Lys Thr Ile Thr Thr Thr Glu Ile Met Asn
565 570 575

Lys Pro Glu Glu Thr Ala Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys
580 585 590

Ala Thr Thr Pro Lys Pro Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro
595 600 605

Thr Ser Thr Lys Lys Pro Lys Thr Met Pro Arg Val Arg Lys Pro Lys
610 615 620

Thr Thr Pro Thr Pro Arg Lys Met Thr Ser Thr Met Pro Glu Leu Asn
625 630 635 640

Pro Thr Ser Arg Ile Ala Glu Ala Met Leu Gln Thr Thr Arg Pro
645 650 655

Asn Gln Thr Pro Asn Ser Lys Leu Val Glu Val Asn Pro Lys Ser Glu
660 665 670

Asp Ala Gly Gly Ala Glu Gly Glu Thr Pro His Met Leu Leu Arg Pro
675 680 685

His Val Phe Met Pro Glu Val Thr Pro Asp Met Asp Tyr Leu Pro Arg
690 695 700

Val Pro Asn Gln Gly Ile Ile Ile Asn Pro Met Leu Ser Asp Glu Thr
705 710 715 720

Asn Ile Cys Asn Gly Lys Pro Val Asp Gly Leu Thr Thr Leu Arg Asn
725 730 735

Gly Thr Leu Val Ala Phe Arg Gly His Tyr Phe Trp Met Leu Ser Pro
740 745 750

Phe Ser Pro Pro Ser Pro Ala Arg Arg Ile Thr Glu Val Trp Gly Ile
755 760 765

Pro Ser Pro Ile Asp Thr Val Phe Thr Arg Cys Asn Cys Glu Gly Lys
770 775 780

Thr Phe Phe Phe Lys Asp Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile
785 790 795 800

Lys Asp Ala Gly Tyr Pro Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu
805 810 815

Thr Gly Gln Ile Val Ala Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp
820 825 830

Pro Glu Ser Val Tyr Phe Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr
835 840 845

Ile Tyr Lys Gln Glu Pro Val Gln Lys Cys Pro Gly Arg Arg Pro Ala
 850 855 860

Leu Asn Tyr Pro Val Tyr Gly Glu Met Thr Gln Val Arg Arg Arg Arg
 865 870 875 880

Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His Thr Ile Arg Ile Gln
 885 890 895

Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys Gly Val Leu His Asn
 900 905 910

Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu Pro Asn Val Val Thr
 915 920 925

Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr
 930 935 940

Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg
 945 950 955 960

Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val
 965 970 975

Trp Tyr Asn Cys Pro
 980

<210> 8
<211> 157
<212> DNA
<213> Artificial

<220>
<223> Lub:1 DNA insert from synthetic cDNA cassette-1.

<400> 8
g c g c g c c c a c a a t c c a a a a g a g c c g c a c c t a c c a c g a c a a a g a g g c c a g c a g a c g a c t a c t a a a g a c c c g c a c c c a c g c c t a c t a c a c a c g a a a c c g g c a c c a a c c a c t c c g g a 60
c c a a a g a g g c c a g c g c c g a c g a c t a c t a a a g a c c c g c a c c a c g c c t a c t a c a c a c g a a a c c g g c a c c a a c c a c t c c g g a 120
c t c c t a c t a c a a c g a a a c c g g c a c c a a c c a c t c c g g a 157

<210> 9
<211> 51
<212> PRT
<213> Artificial

<220>
<223> 51 amino acids encoded by Lub:1 DNA insert (4 KEPAPTT sequences between S373 to E425 in SEQ ID NO: 7).

<400> 9

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro
 35 40 45

Thr Thr Pro
 50

<210> 10
 <211> 3024
 <212> DNA
 <213> Artificial

<220>

<223> Recombinant PRG4-Lub:2 cDNA construct.

<400> 10		
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgttt cgtgattcag	60	
caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaaagg gtattctaga	120	
gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc	180	
aagagagtct gcactgcgga gcttcctgt aaaggccgct gctttgagtc cttcgagaga	240	
gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat	300	
gagagtttct gtgcagaagt gcataatccc acatcaccac catttcaaa gaaagcacct	360	
ccaccccttag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca	420	
aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt	480	
tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgctc gacaatttg	540	
aaaatcaagt cttccaaaaaa tttagctgct aatagagaat tacagaaga actcaaagta	600	
aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat	660	
gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc	720	
acccaacaca ataaagtctag cacatctccc aagatcacaa cagaaaaacc aataaatccc	780	
agaccctagtc ttccaccaa ttctgataca tctaaagaga cgtctttgac agtgaataaa	840	
gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga	900	
aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat	960	
ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa	1020	
ggccctgctc tcaccactcc caaggagccc acgccccacca ctcccaagga gcctgcattct	1080	
accacaccca aagagccac acctaccacc atcaagagcg cgcccacaac tccaaaagag	1140	
ccgcaccta ccacgacaaa gtcagctcct actacgcccc aagagccagc gccgacgact	1200	

actaaagaac	cggcacccac	cacgcctaaa	gaaccagccc	ctactacgac	aaaggagcct	1260
gcacccacaa	ccacgaagag	cgcacccaca	acaccaaagg	agccggcccc	tacgactcct	1320
aaggaaccca	aaccggcacc	aaccactccg	gaaacacctc	ctccaaccac	ttcagaggtc	1380
tctactccaa	ctaccaccaa	ggagcctacc	actatccaca	aaagccctga	tgaatcaact	1440
cctgagctt	ctgcagaacc	cacaccaaaa	gctttgaaa	acagtcccaa	ggaacctggt	1500
gtacctacaa	ctaagacgcc	ggcggcgact	aaacctgaaa	tgactacaac	agctaaagac	1560
aagacaacag	aaagagactt	acgtactaca	cctgaaacta	caactgctgc	acctaagatg	1620
acaaaagaga	cagcaactac	aacagaaaaaa	actaccgaat	ccaaaataac	agctacaacc	1680
acacaagtaa	catctaccac	aactcaagat	accacaccat	tcaaaattac	tactcttaaa	1740
acaactactc	ttgcacccaa	agtaactaca	acaaaaaaga	caattactac	cactgagatt	1800
atgaacaaac	ctgaagaaac	agctaaacca	aaagacagag	ctactaattc	taaagcgaca	1860
actcctaaac	ctcaaaagcc	aaccaaagca	cccaaaaaac	ccacttctac	caaaaagcca	1920
aaaacaatgc	ctagagttag	aaaacccaaag	acgacaccaa	ctccccgcaa	gatgacatca	1980
acaatgccag	aattgaaccc	tacctaaga	atagcagaag	ccatgctcca	aaccaccacc	2040
agacctaacc	aaactccaaa	ctccaaacta	gttgaagtaa	atccaaagag	tgaagatgca	2100
ggtggtgctg	aaggagaaac	acctcatatg	cttctcaggc	ccatgtgtt	catgcctgaa	2160
gttactcccg	acatggatta	cttaccgaga	gtacccaatc	aaggcattat	catcaatccc	2220
atgctttccg	atgagaccaa	tatatgcaat	ggtaagccag	tagatggact	gactacttg	2280
cgcaatggga	cattagttgc	attccgaggt	cattattct	ggatgctaag	tccattcagt	2340
ccaccatctc	cagctcgag	aattactgaa	gtttgggta	ttccttcccc	cattgatact	2400
gtttttacta	ggtgcaactg	tgaaggaaaa	actttttct	ttaaggattc	tcagttactgg	2460
cgttttacca	atgatataaa	agatgcaggg	tacccaaac	caatttcaa	aggatttggaa	2520
ggactaactg	gacaaatagt	ggcagcgcctt	tcaacagcta	aatataagaa	ctggcctgaa	2580
tctgtgtatt	tttcaagag	aggtggcagc	attcagcagt	atatttataa	acaggaacct	2640
gtacagaagt	gccctggaag	aaggcctgct	ctaaattatc	cagtgtatgg	agaaatgaca	2700
caggttagga	gacgtcgctt	tgaacgtgct	ataggacctt	ctcaaacaca	caccatcaga	2760
attcaatatt	cacctgcccag	actggcttat	caagacaaag	gtgtccttca	taatgaagtt	2820
aaagtgagta	tactgtggag	aggacttcca	aatgtggta	cctcagctat	atcactgccc	2880
aacatcagaa	aacctgacgg	ctatgattac	tatgcctttt	ctaaagatca	atactataac	2940
attgatgtgc	ctagtagaac	agcaagagca	attactactc	gttctggca	gaccttatcc	3000

aaagtctggc acaactgtcc ttac

3024

<210> 11
<211> 1007
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of entire PRG4-LUB:2 protein.

<400> 11

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val
1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145 150 155 160

Ser Glu Asn Gln Glu Ser
165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225 230 235 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
245 250 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
260 265 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
275 280 285

Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
290 295 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305 310 315 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
325 330 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
340 345 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
355 360 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
370 375 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385 390 395 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
405 410 415

Thr Lys Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro
420 425 430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr
435 440 445

Thr Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr
450 455 460

Thr Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr
465 470 475 480

Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro
485 490 495

Lys Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro
500 505 510

Glu Met Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg
515 520 525

Thr Thr Pro Glu Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr
530 535 540

Ala Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr
545 550 555 560

Thr Gln Val Thr Ser Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile
565 570 575

Thr Thr Leu Lys Thr Thr Leu Ala Pro Lys Val Thr Thr Lys
580 585 590

Lys Thr Ile Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala
595 600 605

Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro
610 615 620

Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro
625 630 635 640

Lys Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg
645 650 655

Lys Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala
660 665 670

Glu Ala Met Leu Gln Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser
675 680 685

Lys Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu
690 695 700

Gly Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu
705 710 715 720

Val Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile
725 730 735

Ile Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys
740 745 750

Pro Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe
755 760 765

Arg Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro
770 775 780

Ala Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr
785 790 795 800

Val Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp
805 810 815

Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro
820 825 830

Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala
835 840 845

Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe
850 855 860

Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro

865	870	875	880
Val Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr			
885		890	895
Gly Glu Met Thr Gln Val Arg Arg Arg Phe Glu Arg Ala Ile Gly			
900		905	910
Pro Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu			
915		920	925
Ala Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile			
930		935	940
Leu Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro			
945		950	955
Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp			
965		970	975
Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr			
980		985	990
Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro			
995		1000	1005

<210> 12

<211> 235

<212> DNA

<213> Artificial

<220>

<223> Lub:2 DNA insert from synthetic cDNA cassette-1 and one synthetic cDNA cassette-2 sequence.

<400> 12

gcgcgcccac aactccaaaa gagccgcac ctaccacgac aaagtcagct cctactacgc 60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120

ccccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa 180

aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact ccgga 235

<210> 13

<211> 77

<212> PRT

<213> Artificial

<220>

<223> 77 amino acids encoded by Lub:2 DNA insert (6 KEPAPTT sequences between S373 and E451 in SEQ ID NO: 11).

<400> 13

Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala
1				5				10				15			

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
 50 55 60

Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 65 70 75

<210> 14

<211> 3117

<212> DNA

<213> Artificial

<220>

<223> Recombinant PRG4-Lub:3 cDNA construct.

<400> 14

atggcatgga aaacacttcc catttacctg ttgttgctgc tgcgtgttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gcttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300

gagagttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccacccatcg gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtccctc ctccagtagc agttcaagta gttcgctgac gacaattttgg 540

aaaatcaagt cttccaaaaaa tttagctgct aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggta caactcctga cacgtctacc 720

acccaacaca ataaagtctcg cacatctccc aagatcacaa cagcaaaacc aataaatccc 780

agacccagtc ttccaccaa ttctgataca tctaaagaga cgtcttgac agtgaataaa 840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgtatgga 900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaa 1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatt 1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag	1140
cccgcaccta ccacgacaaa gtcagctcct actacgccc aagagccagc gccgacgact	1200
actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct	1260
gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct	1320
aaagaaccag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc	1380
acaacaccaa aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact	1440
ccggaaacac ctcctccaac cacttcagag gtctctactc caactaccac caaggagcct	1500
accactatcc acaaaagccc tcatgtaatca actcctgagc tttctgcaga acccacaacca	1560
aaagctcttg aaaacagtcc caaggaacct ggtgtaccta caactaagac gccggcggcg	1620
actaaacctg aatgactac aacagctaaa gacaagacaa cagaaagaga cttacgtact	1680
acacctgaaa ctacaactgc tgcacctaag atgacaaaag agacagcaac tacaacagaa	1740
aaaactaccg aatccaaaat aacagctaca accacacaag taacatctac cacaactcaa	1800
gataccacac cattcaaaat tactactttt aaaacaacta ctcttgccacc caaagtaact	1860
acaacaaaaa agacaattac taccactgag attatgaaca aacctgaaga aacagctaaa	1920
ccaaaagaca gagctactaa ttctaaagcg acaactccctaa aacctcaaaa gccaacccaaa	1980
gcacccaaaa aacccacttc taccaaaaag ccaaaaacaa tgccttaggt gagaaaacca	2040
aagacgacac caactccccg caagatgaca tcaacaatgc cagaattgaa ccctacctca	2100
agaatagcag aagccatgct ccaaaccacc accagaccta accaaactcc aaactccaaa	2160
ctagttgaag taaatccaaa gagtgaagat gcaggtggtg ctgaaggaga aacacctcat	2220
atgcttctca ggccccatgt gttcatgcct gaagttactc ccgacatgga ttacttaccg	2280
agagtaccca atcaaggcat tatcatcaat cccatgcttt ccgatgagac caatatatgc	2340
aatggtaagc cagtagatgg actgactact ttgcgaatg ggacattagt tgcattccga	2400
ggtcattatt tctggatgct aagtccattc agtccaccat ctccagctcg cagaattact	2460
gaagtttggg gtattccttc cccatttatgactgttttta cttagtgcaa ctgtgaagga	2520
aaaactttct tcttttaagga ttctcagttac tggcgttta ccaatgataat aaaagatgca	2580
gggtacccca aaccaatttt caaaggattt ggaggactaa ctggacaaat agtggcagcg	2640
ctttcaacag ctaaatataa gaactggcct gaatctgtgt aaaaaaaaaa gagaggtggc	2700
agcattcagc agtataattta taaacaggaa cctgtacaga agtgcctgg aagaaggcct	2760
gctctaaattt atccagtgtt tggagaaatg acacaggtt ggagacgtcg ctttgaacgt	2820
gctataggac cttctcaaac acacaccatc agaattcaat attcacctgc cagactggct	2880

tatcaagaca aagggtgcct tcataatgaa gttaaagtga gtatactgtg gagaggactt	2940
ccaaatgtgg ttacctcagc tataatcactg cccaacatca gaaaacctga cggctatgtat	3000
tactatgcct tttctaaaga tcaatactat aacattgtatg tgcctagtag aacagcaaga	3060
gcaattacta ctcgttctgg gcagaccta tccaaagtct ggtacaactg tccttaa	3117

<210> 15
<211> 1038
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of entire PRG4-LUB:3 protein

<400> 15

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val			
1	5	10	15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly		
20	25	30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr		
35	40	45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys		
50	55	60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg			
65	70	75	80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys		
85	90	95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser		
100	105	110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr		
115	120	125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys		
130	135	140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val			
145	150	155	160

Ser Glu Asn Gln Glu Ser		
165	170	175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg		
180	185	190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr		
195	200	205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225 230 235 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
245 250 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
260 265 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
275 280 285

Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
290 295 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305 310 315 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
325 330 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
340 345 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
355 360 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
370 375 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385 390 395 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
405 410 415

Thr Lys Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro
420 425 430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
435 440 445

Lys Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
450 455 460

Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr
465 470 475 480

Pro Glu Thr Pro Pro Pro Thr Ser Glu Val Ser Thr Pro Thr Thr
485 490 495

Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro
500 505 510

Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys
515 520 525

Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu
530 535 540

Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr
545 550 555 560

Thr Pro Glu Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala
565 570 575

Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr
580 585 590

Gln Val Thr Ser Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr
595 600 605

Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys
610 615 620

Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys
625 630 635 640

Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln
645 650 655

Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys
660 665 670

Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys
675 680 685

Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu
690 695 700

Ala Met Leu Gln Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys
705 710 715 720

Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly
725 730 735

Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val
740 745 750

Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile
755 760 765

Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro
770 775 780

Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg
785 790 795 800

Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala
805 810 815

Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val
820 825 830

Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Lys Asp Ser

835

840

845

Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys
 850 855 860

Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala
 865 870 875 880

Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe
 885 890 895

Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val
 900 905 910

Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly
 915 920 925

Glu Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro
 930 935 940

Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala
 945 950 955 960

Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu
 965 970 975

Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn
 980 985 990

Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp Gln
 995 1000 1005

Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr
 1010 1015 1020

Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro
 1025 1030 1035

<210> 16

<211> 328

<212> DNA

<213> Artificial

<220>

<223> Lub:3 DNA insert from synthetic cDNA cassette-1 and two synthetic cDNA cassette-2 sequences.

<400> 16

gcgcgccccac aactccaaaa gagccgcac ctaccacgac aaagttagct cctactacgc 60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa 180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240

ccacaaccac gaagagcgcac cccacaacac caaaggagcc ggcccctacg actcctaagg 300

aacccaaacc ggcaccaacc actccgg'a

328

<210> 17

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 108 amino acids encoded by Lub:3 DNA insert (9 KEPAPTT sequences between S373 and E482 in SEQ ID NO: 15)

<400> 17

Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala
1				5					10				15		

Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala
	20					25						30			

Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala
	35					40						45			

Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro
	50				55					60					

Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala	Pro
	65				70						75		80		

Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	
	85					90						95			

Thr	Pro	Lys	Glu	Pro	Lys	Pro	Ala	Pro	Thr	Thr	Pro
	100					105					

<210> 18

<211> 3210

<212> DNA

<213> Artificial

<220>

<223> recombinant PRG4-Lub:4 cDNA construct.

<400> 18

atggcatgga	aaacacttcc	catttacctg	ttgttgctgc	tgtctgtttt	cgtgattcag	60
caagtttcat	ctcaagattt	atcaagctgt	gcagggagat	gtggggaaagg	gtattctaga	120
gatgccacct	gcaactgtga	ttataactgt	caacactaca	tggagtgctg	ccctgatttc	180
aagagagtct	gcactgcgga	gctttcctgt	aaaggccgct	gctttgagtc	cttcgagaga	240
gggagggagt	gtgactgcga	cgcctaattgt	aagaagtatg	acaagtgctg	tcccgattat	300
gagagtttct	gtgcagaagt	gcataatccc	acatcaccac	catcttcaaa	gaaagcacct	360
ccacccatcag	gagcatctca	aaccatcaaa	tcaacaacca	aacgttccacc	caaaccacca	420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt	480
tctgaaaatc aagagtccctc ctccagtagc agttcaagta gttcgctgac gacaatttgg	540
aaaatcaagt cttccaaaaa tttagctgct aatagagaat tacagaagaa actcaaagta	600
aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgttagat	660
gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc	720
acccaacaca ataaagttag cacatctccc aagatcacaa cagaaaaacc aataaatccc	780
agaccaggc ttccaccta ttctgataca tctaaagaga cgtctttgac agtgaataaa	840
gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga	900
aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat	960
ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaacccaa	1020
ggccctgctc tcaccactcc caaggagccc acgccccacca ctcccaagga gcctgcatct	1080
accacaccca aagagccac acctaccacc atcaagagcg cgccccacaac tccaaaagag	1140
cccgcaccta ccacgacaaa gtcagctcct actacgccc aagagccagc gccgacgact	1200
actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct	1260
gcacccacca ccacgaagag cgacccaca acaccaaagg agccggcccc tacgactcct	1320
aaagaaccaag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc	1380
acaacaccaa aggagccgc ccctacgact cctaaagaac cagccccctac tacgacaaag	1440
gagcctgac ccacaaccac gaagagcgca cccacaacac caaaggagcc ggccccctacg	1500
actcctaagg aacccaaacc ggcaccaacc actccggaaa cacctcctcc aaccacttca	1560
gaggtctcta ctccaaactac caccaaggag cctaccacta tccacaaaag ccctgatgaa	1620
tcaactcctg agctttctgc agaacccaca cccaaagctc ttgaaaacag tcccaaggaa	1680
cctggtgtac ctacaactaa gacgcggcg gcgactaac ctgaaatgac tacaacagct	1740
aaagacaaga caacagaaag agacttacgt actacacctg aaactacaac tgctgcaccc	1800
aagatgacaa aagagacagc aactacaaca gaaaaaacta cggaaatccaa aataacagct	1860
acaaccacac aagtaacatc taccacaact caagatacca caccattcaa aattactact	1920
cttaaaaacaa ctactctgc acccaaagta actacaacaa aaaagacaat tactaccact	1980
gagattatga acaaaccctga agaaacagct aaacccaaaag acagagctac taattctaaa	2040
gcgacaactc ctaaacctca aaagccaaacc aaagcacccca aaaaacccac ttctacccaa	2100
aagccaaaaa caatgcctag agtgagaaaa ccaaagacga caccaactcc ccgcaagatg	2160
acatcaacaa tgccagaatt gaaccctacc tcaagaatag cagaagccat gctccaaacc	2220

accaccagac ctaaccaaac tccaaactcc aaactagtt aagtaaatcc aaagagtcaa	2280
gatgcagggt gtgctgaagg agaaacaccc catatgcttc tcaggccccca tgtgttcatg	2340
cctgaagtta ctcccgacat ggattactta ccgagagtac ccaatcaagg cattatcatc	2400
aatcccatgc tttccgatga gaccaatata tgcaatggta agccagtaga tggactgact	2460
actttgcgca atggacatt agttgcattc cgaggtcatt atttctggat gctaagtcca	2520
ttcagtcac catctccagc tcgcagaatt actgaagttt ggggtattcc ttccccatt	2580
gatactgttt ttacttaggtg caactgtgaa ggaaaaactt tcttctttaa ggattctcag	2640
tactggcggtt ttaccaatga tataaaagat gcagggtacc ccaaaccaat tttcaaagga	2700
tttggaggac taactggaca aatagtggca gcgcattcaa cagctaaata taagaactgg	2760
cctgaatctg tgtatTTTTT caagagaggt ggcagcattc agcagtatat ttataaacag	2820
gaacctgtac agaagtgcgg tggagaagg cctgctctaa attatccagt gtatggagaa	2880
atgacacagg ttaggagacg tcgcTTTgaa cgtgctatag gaccttctca aacacacacc	2940
atcagaattc aatattcacc tgccagactg gcttatcaag acAAAGGTGT ctttcataat	3000
gaagttaaag tgagtatact gtggagagga cttccaaatg tggttacctc agctatatca	3060
ctgcccaca tcagaaaacc tgacggctat gattactatg cttttctaa agatcaatac	3120
tataacattt atgtgcctag tagaacagca agagcaatta ctactcggtc tggcagacc	3180
ttatccaaag tctggtacaa ctgtccttaa	3210

<210> 19

<211> 1069

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of entire PRG4-LUB:4 protein.

<400> 19

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val			
1	5	10	15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly		
20	25	30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr		
35	40	45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys		
50	55	60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg

65

70

75

80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
 85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
 100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
 115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
 130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
 145 150 155 160

Ser Glu Asn Gln Glu Ser
 165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
 180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
 195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
 210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
 225 230 235 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
 245 250 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
 260 265 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
 275 280 285

Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
 290 295 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
 305 310 315 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
 325 330 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
 340 345 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
 355 360 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 370 375 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 385 390 395 400
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 405 410 415
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
 420 425 430
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
 435 440 445
 Lys Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
 450 455 460
 Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys
 465 470 475 480
 Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
 485 490 495
 Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 500 505 510
 Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr
 515 520 525
 Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu
 530 535 540
 Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu
 545 550 555 560
 Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met
 565 570 575
 Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr
 580 585 590
 Pro Glu Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr
 595 600 605
 Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Gln
 610 615 620
 Val Thr Ser Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr
 625 630 635 640
 Leu Lys Thr Thr Leu Ala Pro Lys Val Thr Thr Lys Lys Thr
 645 650 655
 Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro
 660 665 670
 Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys
 675 680 685
 Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr
 690 695 700

Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met
 705 710 715 720
 Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala
 725 730 735
 Met Leu Gln Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu
 740 745 750
 Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu
 755 760 765
 Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr
 770 775 780
 Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile
 785 790 795 800
 Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val
 805 810 815
 Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly
 820 825 830
 His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg
 835 840 845
 Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe
 850 855 860
 Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Lys Asp Ser Gln
 865 870 875 880
 Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro
 885 890 895
 Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu
 900 905 910
 Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys
 915 920 925
 Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln
 930 935 940
 Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu
 945 950 955 960
 Met Thr Gln Val Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser
 965 970 975
 Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr
 980 985 990
 Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu Trp
 995 1000 1005
 Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn

1010	1015	1020
Ile Arg Lys Pro Asp Gly Tyr	Asp Tyr Tyr Ala Phe Ser Lys Asp	
1025	1030	1035
Gln Tyr Tyr Asn Ile Asp Val	Pro Ser Arg Thr Ala Arg Ala Ile	
1040	1045	1050
Thr Thr Arg Ser Gly Gln Thr	Leu Ser Lys Val Trp Tyr Asn Cys	
1055	1060	1065

Pro

<210> 20
<211> 421
<212> DNA
<213> Artificial

<220>
<223> Lub:4 DNA insert from cDNA cassette-1 and three synthetic cDNA cassette-2 sequences.

<400> 20	gcgcccccac aactccaaaa gagccgcac ctaccacgac aaagttagct cctactacgc	60
	ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag	120
	ccccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa	180
	aggagccggc ccctacgact cctaaagaac cagccctac tacgacaaag gagcctgcac	240
	ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaaag	300
	aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc gcacccacaa	360
	caccaaagga gccggccct acgactccta aggaacccaa accggcacca accactccgg	420
a		421

<210> 21
<211> 139
<212> PRT
<213> Artificial

<220>
<223> 139 amino acids encoded by Lub:4 DNA insert (12 KEPAPTT sequences between S373 and E513 in SEQ ID NO: 19)

<400> 21

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala			
1	5	10	15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala		
20	25	30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
 50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala Pro
 65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 85 90 95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala Pro Thr
 100 105 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 115 120 125

Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 130 135

<210> 22

<211> 3303

<212> DNA

<213> Artificial

<220>

<223> Recombinant PRG4-Lub:5 cDNA construct

<400> 22

atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccacccctcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgac gacaatttgg 540

aaaatcaagt cttccaaaaa ttcaagtcgtct aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgttagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720

acccaacaca ataaagtctcag cacatctccc aagatcacaa cagcaaaacc aataaatccc 780

agaccacagtc ttccacctaa ttctgataca tctaaagaga cgtcttgac agtgaataaa 840

gagacaacag ttgaaactaa agaaaactact acaacaaata aacagacttc aactgtatgga	900
aaagagaaga ctacttccgc taaagagaca caaagtatacg agaaaacatc tgctaaagat	960
ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa	1020
ggccctgctc tcaccactcc caaggagccc acgcccacca ctccccagga gcctgcattct	1080
accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag	1140
cccgaccta ccacgacaaa gtcagctcct actacgccc aagagccagc gccgacgact	1200
actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct	1260
gcacccaccaa ccacgaagag cgacccacca acaccaaagg agccggcccc tacgactcct	1320
aaagaaccag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc	1380
acaacaccaa aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag	1440
gagcctgcac ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg	1500
actcctaaag aaccagcccc tactacgaca aaggagcctg caccacaaac cacgaagagc	1560
gcacccaccaa caccaaaagga gccggccct acgactccta aggaacccaa accggcacca	1620
accactccgg aaacaccctcc tccaaccact tcagaggctc ctactccaaac taccaccaag	1680
gagcctacca ctatccacaa aagccctgat gaatcaactc ctgagcttc tgcagaaccc	1740
acacaaaaag ctctgaaaaa cagtcacaaag gaacctggtg tacctacaac taagacgccc	1800
gcggcgacta aacctgaaat gactacaaca gctaaagaca agacaacaga aagagactta	1860
cgtactacac ctgaaactac aactgctgca cctaagatga caaaagagac agcaactaca	1920
acagaaaaaa ctaccgaatc caaaataaca gctacaacca cacaagtaac atctaccaca	1980
actcaagata ccacaccatt caaaattact actctaaaa caactactct tgacccacaa	2040
gtaactacaa caaaaagac aattactacc actgagatta tgaacaaacc tgaagaaaca	2100
gctaaaccaa aagacagagc tactaattct aaagcgacaa ctcctaaacc tcaaaagcc	2160
accaaagcac ccaaaaaacc cacttctacc aaaaagccaa aaacaatgcc tagagtgaga	2220
aaacccaaaga cgacaccaac tccccgcaag atgacatcaa caatgccaga attgaaccct	2280
acctcaagaa tagcagaagc catgctccaa accaccacca gacctaacca aactccaaac	2340
tccaaactag ttgaagtaaa tccaaagagt gaagatgcag gtggtgctga aggagaaaca	2400
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ttacccgagag taccatatca aggcattatc atcaatccca tgctttccga tgagaccaat	2520
atatgcaatg gtaagccagt agatggactg actactttgc gcaatgggac attagttgca	2580
ttccgaggc attatttctg gatgctaagt ccattcagtc caccatctcc agctcgcaga	2640

attactgaag tttggggtat tccttccccc attgatactg ttttactag gtgcaactgt	2700
gaaggaaaaa ctttcttc tttaaggattct cagtaactggc gttttaccaa tgatataaaa	2760
gatgcagggt accccaaacc aattttcaaa ggatttggag gactaactgg acaaatacg	2820
gcagcgcttt caacagctaa atataagaac tggcctgaat ctgtgtattt tttcaagaga	2880
ggtggcagca ttcagcagta tatttataaa caggaacctg tacagaagtg ccctggaaga	2940
aggcctgctc taaatttatcc agtgtatgga gaaatgacac aggttaggag acgtcgctt	3000
gaacgtgcta taggaccttc tcaaacacac accatcagaa ttcaatattc acctgccaga	3060
ctggcttatac aagacaaagg tgtccttcat aatgaagttt aagttagtat actgtggaga	3120
ggacttccaa atgtggttac ctcaagctata tcactgccc acatcagaaa acctgacggc	3180
tatgattact atgcctttc taaaagatcaa tactataaca ttgatgtgcc tagtagaaca	3240
gcaagagcaa ttactactcg ttctggcag accttatcca aagtctggta caactgtcct	3300
taa	3303

<210> 23

<211> 1100

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of entire PRG4-LUB:5 protein.

<400> 23

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val			
1	5	10	15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly		
20	25	30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr		
35	40	45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys		
50	55	60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg			
65	70	75	80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys		
85	90	95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser		
100	105	110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr		
115	120	125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145 150 155 160

Ser Glu Asn Gln Glu Ser
165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225 230 235 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
245 250 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
260 265 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
275 280 285

Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
290 295 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305 310 315 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
325 330 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
340 345 350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
355 360 365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
370 375 380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385 390 395 400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
405 410 415

Thr Lys Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro
420 425 430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr

435	440	445
Lys Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys 450	455	460
Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys 465	470	475
Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu 485	490	495
Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu 500	505	510
Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro 515	520	525
Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro Glu 530	535	540
Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr Lys 545	550	555
Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu 565	570	575
Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro 580	585	590
Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr 595	600	605
Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro 610	615	620
Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr 625	630	635
Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val 645	650	655
Thr Ser Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu 660	665	670
Lys Thr Thr Leu Ala Pro Lys Val Thr Thr Lys Lys Thr Ile 675	680	685
Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys 690	695	700
Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro 705	710	715
Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met 725	730	735
Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr 740	745	750

Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met
 755 760 765
 Leu Gln Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val
 770 775 780
 Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr
 785 790 795 800
 Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro
 805 810 815
 Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn
 820 825 830
 Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp
 835 840 845
 Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly His
 850 855 860
 Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg Arg
 865 870 875 880
 Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe Thr
 885 890 895
 Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln Tyr
 900 905 910
 Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro Ile
 915 920 925
 Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu Ser
 930 935 940
 Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys Arg
 945 950 955 960
 Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln Lys
 965 970 975
 Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu Met
 980 985 990
 Thr Gln Val Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser Gln
 995 1000 1005
 Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr
 1010 1015 1020
 Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu
 1025 1030 1035
 Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro
 1040 1045 1050
 Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys
 1055 1060 1065

Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala
 1070 1075 1080

Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn
 1085 1090 1095

Cys Pro
 1100

<210> 24

<211> 514

<212> DNA

<213> Artificial

<220>

<223> Lub:5 DNA insert from cDNA cassette-1 and four synthetic cDNA cassette-2 sequences

<400> 24

gcgcccccac aactccaaaa gagccgcac ctaccacgac aaagttagct cctactacgc	60
ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgct aaagaaccag	120
ccccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa	180
aggagccggc ccctacgact cctaaagaac cagccctac tacgacaaag gagcctgcac	240
ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaaag	300
aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc gcacccacaa	360
caccaaagga gccggccct acgactccta aagaaccagc ccctactacg acaaaggagc	420
ctgcacccac aaccacgaaag agcgcaccca caacacaaa ggagccggcc cttacgactc	480
ctaaggaacc caaaccggca ccaaccactc cgga	514

<210> 25

<211> 170

<212> PRT

<213> Artificial

<220>

<223> 170 amino acids encoded by Lub:5 DNA insert (15 KEPAPTT sequences between S373 and E544 in SEQ ID NO: 23)

<400> 25

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala			
1	5	10	15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala		
20	25	30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala		
35	40	45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
 50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala Pro
 65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 85 90 95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala Pro Thr
 100 105 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 115 120 125

Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala Pro Thr Thr
 130 135 140

Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
 145 150 155 160

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 165 170

<210> 26

<211> 45

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence "APTPKEPAPTTKSAPTPKEPAPTT
KEPAPTPKEPAPTTK" (45 amino acids) in preferred PRG4-LUB:N
protein

<400> 26

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Ser Ala
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys Glu Pro Ala
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Lys
 35 40 45

<210> 27

<211> 31

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence "KEPAPTTKEPAPTTKSAPTPKEPAPTP" (31 amino
acids) repeated N-1 times in preferred PRG4-LUB:N protein

<400> 27

40

Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr Thr
1 5 10 15

Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
20 25 30

<210> 28

<211> 22

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence "EPAPTTKSAPTPKEPAPTP" (22 amino acids) joining SEQ ID NO: 26 to (N-2) repeats of SEQ ID NO: 27 in preferred PRG4-LUB:N protein where N = 3 or more.

<400> 28

Glu Pro Ala Pro Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
1 5 10 15

Pro Ala Pro Thr Thr Pro
20

<210> 29

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence "KEPKPAPTP" (10 amino acids) in preferred PRG4-LUB:N protein where N = 2 or more.

<400> 29

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
1 5 10